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EXAMINER	
DUNSTON, JENNIFER ANN	
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/538,532	VAN DER VOSSEN ET AL.	
	Examiner	Art Unit	
	Jennifer Dunston	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-33* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4 and 7-33* is/are rejected.

7)☒ Claim(s) *5 and 6* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *24 March 2006* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *6/10/2005; 4/23/2007*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Receipt is acknowledged of an amendment, filed 6/10/2005, in which claims 4-7, 9, 10, 12 and 13 were amended, and claims 14-33 were newly added. Currently, claims 1-33 are pending and under consideration.

Priority

Acknowledgment is made of applicant's claim for foreign priority under 35 U.S.C. 119(a)-(d). Receipt of the certified copy of the foreign priority document, Netherlands 1022152, is acknowledged. These papers have been placed of record in the file.

Information Disclosure Statement

Receipt of information disclosure statements, filed on 6/10/2005 and 4/23/2007, is acknowledged. The signed and initialed PTO 1449s have been mailed with this action.

Drawings

The drawings are objected to because they are not legible and will not reproduce well. Figures 1-3 are black boxes, and the details of the gels cannot be seen. Corrected drawing sheets in compliance with 37 CFR 1.121(d) are required in reply to the Office action to avoid abandonment of the application. Any amended replacement drawing sheet should include all of the figures appearing on the immediate prior version of the sheet, even if only one figure is being amended. The figure or figure number of an amended drawing should not be labeled as "amended." If a drawing figure is to be canceled, the appropriate figure must be removed from

the replacement sheet, and where necessary, the remaining figures must be renumbered and appropriate changes made to the brief description of the several views of the drawings for consistency. Additional replacement sheets may be necessary to show the renumbering of the remaining figures. Each drawing sheet submitted after the filing date of an application must be labeled in the top margin as either "Replacement Sheet" or "New Sheet" pursuant to 37 CFR 1.121(d). If the changes are not accepted by the examiner, the applicant will be notified and informed of any required corrective action in the next Office action. The objection to the drawings will not be held in abeyance.

Claim Objections

Claims 5 and 6 are objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim should refer to other claims in the alternative only. See MPEP § 608.01(n). Accordingly, claims 5 and 6 have not been further treated on the merits.

Double Patenting

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and In *re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting

ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 1-4, 10-15 and 26-33 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-13 of copending Application No. 10/511,496 (hereinafter the '496 application) in view of Mirzabekov et al (US Patent No. 6,458,584 B1; see the entire reference).

Although the conflicting claims are not identical, they are not patentably distinct from each other because claims 1-3 are generic to all that is recited in claims 1-13 of the '496 application. That is, claims 1-13 of the '496 application fall entirely with the scope of claims 1-3 of the instant application or, in other words, instant claims 1-3 are anticipated by claims 1-13 of the '496 application. Specifically, the conflicting claims are narrower in scope than the instant claims in that they require the step of qualitatively or quantitatively detecting a plurality of different biomolecules in one or more microorganisms. Further, conflicting claim 4 anticipates instant claims 4, 14 and 15. Moreover, conflicting claims 8-11 anticipated instant claims 10-13 and 26-33 for the same reasons set forth above.

With respect to instant claims 7-9 and 16-25 the instant claims are drawn to measuring the composition of a microbial population by using taxon-specific nucleic acid markers and microarrays. The conflicting claims require the measurement of a microbial population by detecting qualitatively or quantitatively a plurality of different biomolecules. However, the conflicting claims do not specifically limit the detecting to the use of taxon-specific biomolecules. Mirzabekov et al teach a method for determining an environmental condition,

comprising measuring genetic sequences in a microbial sample isolated from air, water, soil, blood, cells, tissue, tissue culture or food, where the measured genetic sequences allow the typing of the microbial organisms present (e.g., Abstract; column 5, line 17 to column 6, line 27). Mirzabekov et al teach the method wherein taxon-specific markers such as 16S rRNA sequences are used to measure sequence diversity of the nucleic acids (e.g., column 6, lines 8-27; Examples 5, 9 and 10). Mirzabekov et al teach the method where the detection of the taxon-specific markers such as 16S rRNA is detected by means of one or more microarrays (e.g., column 9, line 20 to column 10, line 62). Mirzabekov et al teach that the use of oligonucleotide microarrays allows efficient, reliable evaluation of microorganisms present in a sample, where the evaluation is either qualitative or quantitative (e.g., column 10, lines 39-62). Thus, it would have been obvious to one of ordinary skill in the art at the time the invention was made, to use the oligonucleotide microarrays for detecting qualitatively a plurality of different 16S rRNA biomolecules in the claimed method of the '496 application to result in the predictable outcome of measuring a composition of a microbial population.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1, 2, 4, 7, 8, 10-14, 16, 17, 19, 26, 28, 30 and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Welling et al (WO 97/05282, cited on the IDS filed 4/23/2007; see the entire reference).

Regarding claim 1, Welling et al teach a method comprising measuring a composition of a microbial population exposed to an environmental condition by using fluorescence *in situ* hybridization where oligonucleotide probes to 16S rRNA are hybridized to samples of intestinal microflora (e.g., Abstract; page 8, line 20 to page 9, line 7; page 24).

Regarding claim 2, Welling et al teach a method comprising measuring a composition of a microbial population exposed to an environmental condition by using fluorescence *in situ* hybridization where oligonucleotide probes to 16S rRNA are hybridized to samples of intestinal microflora, and where the method is used to measure changes in the composition of the microbial population (e.g., Abstract; page 6, line 21 to page 7, line 21; page 8, line 20 to page 9, line 7; page 24).

Regarding claim 4, Welling et al teach the method where the microbial population comprises bacteria (e.g., pages 18-21; Tables 1 and 2).

Regarding claims 7 and 8, Welling et al teach the method where the oligonucleotide probes are taxon-specific markers (e.g., pages 18-21; Tables 1 and 2).

Regarding claims 10-13, Welling et al teach the claimed method step of measuring a composition of a microbial population which has been exposed to an environmental condition. Specifically, Welling et al teach a method comprising measuring a composition of a microbial

population exposed to an environmental condition using fluorescence *in situ* hybridization where oligonucleotide probes to 16S rRNA are hybridized to samples of intestinal microflora (e.g., Abstract; page 6, line 21 to page 7, line 21; page 8, line 20 to page 9, line 7; page 24). Thus, Welling et al teach each of the limitations of the rejected claims.

Regarding claim 14, Welling et al teach the method where the microbial population comprises bacteria (e.g., pages 18-21; Tables 1 and 2).

Regarding claim 16, Welling et al teach the method where the oligonucleotide probes are taxon-specific markers (e.g., pages 18-21; Tables 1 and 2).

Regarding claims 17 and 19, Welling et al teach the method where the oligonucleotide probes are taxon-specific markers (e.g., pages 18-21; Tables 1 and 2).

Regarding claims 26, 28, 30 and 32, Welling et al teach the claimed method step of measuring changes in a composition of a microbial population which has been exposed to changes in an environmental condition. Specifically, Welling et al teach using fluorescence *in situ* hybridization where oligonucleotide probes to 16S rRNA are hybridized to samples of intestinal microflora, and where the method is used to measure changes in the composition of the microbial population (e.g., Abstract; page 6, line 21 to page 7, line 21; page 8, line 20 to page 9, line 7; page 24). Thus, Welling et al teach each of the limitations of the rejected claims.

Claims 1, 2, 4, 7-14, 16, 17, 19, 21, 22, 24, 26, 28, 30 and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Rudi et al (Applied and Environmental Microbiology, Vol. 66, No. 9, pages 4004-4011, September 2000; see the entire reference).

Regarding claim 1, Rudi et al teach a method comprising measuring a composition of a microbial population which has been exposed to a lake environment, ranging from localities moderately influenced by plant nutrients (mesotrophic) to lakes heavily affected by plant nutrients (eutrophic), where the measuring is done by hybridizing a nucleic acid sample obtained from bacteria isolated from the lake to a microarray containing partial 16S rDNA sequences covering variable regions of bacterial sequences (e.g., pages 4004-4005).

Regarding claim 2, Rudi et al teach a method comprising measuring a composition of a microbial population which has been exposed to a lake environment, ranging from localities moderately influenced by plant nutrients (mesotrophic) to lakes heavily affected by plant nutrients (eutrophic), where the measuring is done by hybridizing a nucleic acid sample obtained from bacteria isolated from the lake to a microarray containing partial 16S rDNA sequences covering variable regions of bacterial sequences (e.g., pages 4004-4005). Rudi et al teach measuring changes in the composition of the microbial population under the different lake environmental conditions (e.g., Table 1; Figure 4).

Regarding claim 4, Rudi et al teach the method where the microbial population comprises bacteria (e.g., page 4006, Construction and validation of the probes).

Regarding claims 7 and 8, Rudi et al teach the method where the measuring comprises the use of taxon-specific oligonucleotide probes (e.g., page 4006, Construction and validation of the probes).

Regarding claims 9 and 21, Rudi et al teach the method where the taxon-specific oligonucleotide probes are used on a microarray (e.g., page 4005, Probe hybridization and chromogenic detection; Figure 1).

Regarding claims 10-13, Rudi et al teach the claimed method step of measuring a composition of a microbial population which has been exposed to an environmental condition. Specifically, Rudi et al teach measuring a composition of a microbial population which has been exposed to a lake environment, ranging from localities moderately influenced by plant nutrients (mesotrophic) to lakes heavily affected by plant nutrients (eutrophic), where the measuring is done by hybridizing a nucleic acid sample obtained from bacteria isolated from the lake to a microarray containing partial 16S rDNA sequences covering variable regions of bacterial sequences (e.g., pages 4004-4005). Thus, Rudi et al teach each of the limitations of the rejected claims.

Regarding claim 14, Rudi et al teach the method where the microbial population comprises bacteria (e.g., page 4006, Construction and validation of the probes).

Regarding claim 16, Rudi et al teach the method where the measuring comprises the use of taxon-specific oligonucleotide probes (e.g., page 4006, Construction and validation of the probes).

Regarding claims 17 and 19, Rudi et al teach the method where the measuring comprises the use of taxon-specific oligonucleotide probes (e.g., page 4006, Construction and validation of the probes).

Regarding claims 22 and 24, Rudi et al teach the method where the taxon-specific oligonucleotide probes are used on a microarray (e.g., page 4005, Probe hybridization and chromogenic detection; Figure 1).

Regarding claims 26, 28, 30 and 32, Rudi et al teach the claimed method step of measuring changes in a composition of a microbial population which has been exposed to

changes in an environmental condition. Specifically, Rudi et al teach a method comprising measuring a composition of a microbial population which has been exposed to a lake environment, ranging from localities moderately influenced by plant nutrients (mesotrophic) to lakes heavily affected by plant nutrients (eutrophic), where the measuring is done by hybridizing a nucleic acid sample obtained from bacteria isolated from the lake to a microarray containing partial 16S rDNA sequences covering variable regions of bacterial sequences (e.g., pages 4004-4005). Rudi et al teach measuring changes in the composition of the microbial population under the different lake environmental conditions (e.g., Table 1; Figure 4). Thus, Rudi et al teach each of the limitations of the rejected claims.

Claims 1, 4, 7-13, 16 and 21 are rejected under 35 U.S.C. 102(e) as being anticipated by Mirzabekov et al (US Patent No. 6,458,584 B1; see the entire reference).

Regarding claim 1, Mirzabekov et al teach a method for determining an environmental condition, comprising measuring genetic sequences in a microbial sample isolated from air, water, soil, blood, cells, tissue, tissue culture or food, where the measured genetic sequences allow the typing of the microbial organisms present (e.g., Abstract; column 5, line 17 to column 6, line 27).

Regarding claim 4, Mirzabekov et al teach the method where the microbial population comprises bacteria (e.g., column 5, lines 55-59).

Regarding claims 7, 8, 16, Mirzabekov et al teach the method wherein taxon-specific markers such as 16S rRNA sequences are used to measure sequence diversity of the nucleic acids (e.g., column 6, lines 8-27; Examples 5, 9 and 10).

Regarding claims 9 and 21, Mirzabekov et al teach the method where the detection of the taxon-specific markers such as 16S rRNA is detected by means of one or more microarrays (e.g., column 9, line 20 to column 10, line 62).

Regarding claims 10-13, Mirzabekov et al teach the method step of measuring a composition of a microbial population which has been exposed to an environmental condition. Specifically, Mirzabekov et al teach measuring genetic sequences in a microbial sample isolated from air, water, soil, blood, cells, tissue, tissue culture or food, where the measured genetic sequences allow the typing of the microbial organisms present (e.g., Abstract; column 5, line 17 to column 6, line 27). Thus, the teachings of Mirzabekov et al meet each of the limitations of the rejected claims.

Claims 1-4 and 7-33 are rejected under 35 U.S.C. 102(e) as being anticipated by Ashby (US Patent No. 6,613,520 B2; see the entire reference).

Regarding claim 1, Ashby teaches a method for determining an environmental condition by measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29).

Regarding claim 2, Ashby teaches a method for determining an environmental condition by measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29). Ashby

teaches performing the method as a time course to reveal trends in populations over time (e.g., column 14, line 59 to column 15, line 25).

Regarding claim 3, Ashby teaches a method for determining an environmental condition by measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29; column 10, line 5 to column 13, line 67). To analyze the marker data, Ashby teaches the steps of making a database containing reference data files which are collections of diversity profiles that provide an accurate representation of members represent in a particular population, correlating the measured diversity profiles with the profiles in the database for diagnostic purposes, thereby determining a particular environmental condition such as the presence of mineral deposits, petroleum reserves, or microbial contamination of human and animal foodstocks (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 14, line 1 to column 17, line 15; Figures 9 and 10).

Regarding claim 4, Ashby teaches the method where the microbial population comprises bacteria or fungi (e.g., column 9, lines 1-5).

Regarding claims 7 and 8, Ashby teaches the method where the measuring comprises the use of taxon-specific nucleic acid markers (e.g., paragraph bridging columns 3-4; column 9, lines 6-16).

Regarding claim 9, Ashby teaches the method where the marker diversity is measured by hybridizing microbial rDNA to immobilized oligonucleotides in DNA microarrays (e.g., Example 7).

Regarding claims 10-13, Ashby teaches the claimed method step of measuring a composition of a microbial population which has been exposed to an environmental condition. Specifically, Ashby teaches measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29). Thus, the teachings of Ashby meet each of the limitations of the rejected claims.

Regarding claim 14, Ashby teaches the method where the microbial population comprises bacteria or fungi (e.g., column 9, lines 1-5).

Regarding claim 15, Ashby teaches the method where the microbial population comprises bacteria or fungi (e.g., column 9, lines 1-5).

Regarding claim 16, Ashby teaches the method where the measuring comprises the use of taxon-specific nucleic acid markers (e.g., paragraph bridging columns 3-4; column 9, lines 6-16).

Regarding claims 17 and 19, Ashby teaches the method where the measuring comprises the use of taxon-specific nucleic acid markers (e.g., paragraph bridging columns 3-4; column 9, lines 6-16).

Regarding claims 18 and 20, Ashby teaches the method where the measuring comprises the use of taxon-specific nucleic acid markers (e.g., paragraph bridging columns 3-4; column 9, lines 6-16).

Regarding claims 21-25, Ashby teaches the method where the marker diversity is measured by hybridizing microbial rDNA to immobilized oligonucleotides in DNA microarrays (e.g., Example 7).

Regarding claims 26, 28, 30 and 32, Ashby teaches the claimed method step of measuring changes in a composition of a microbial population that has been exposed to changes in an environmental condition. Specifically, Ashby teaches a method for determining an environmental condition by measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29). Ashby teaches performing the method as a time course to reveal trends in populations over time (e.g., column 14, line 59 to column 15, line 25). Thus, the teachings of Ashby meet each of the limitations of the rejected claims.

Regarding claims 27, 29, 31 and 33, Ashby teaches the claimed method steps of (i) measuring a composition of a microbial population which has been exposed to an environmental condition, (ii) correlating said composition to a previously compiled reference data file of a plurality of compositions obtained through exposure of said microbial population to a plurality of environmental conditions, and (iii) determining said environmental condition on the basis of the outcome of said correlation. Specifically, Ashby teaches a method for determining an environmental condition by measuring the marker diversity profile of a microbial population of an environmental sample, where the marker is characteristic of a particular genome in the population of interest (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 9, lines 1-29; column 10, line 5 to column 13, line 67). To analyze the marker data, Ashby teaches the steps of making a database containing reference data files which are collections of diversity profiles that provide an accurate representation of members represent in a particular population, correlating the measured diversity profiles with the profiles in the database

for diagnostic purposes, thereby determining a particular environmental condition such as the presence of mineral deposits, petroleum reserves, or microbial contamination of human and animal foodstocks (e.g., column 3, line 60 to column 4, line 49; column 8, lines 41-56; column 14, line 1 to column 17, line 15; Figures 9 and 10). Thus, the teachings of Ashby meet each of the limitations of the rejected claims.

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jennifer Dunston whose telephone number is 571-272-2916. The examiner can normally be reached on M-F, 9 am to 5 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Joseph Woitach can be reached at 571-272-0739. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Jennifer Dunston, Ph.D.
Examiner
Art Unit 1636

/JD/
/Daniel M Sullivan/
Primary Examiner, Art Unit 1636